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RAW SEQUENCE LISTING

DATE: 12/21/2001

PATENT APPLICATION: US/09/744,226A

TIME: 13:10:09

Input Set : A:\2534seq.txt

Output Set: N:\CRF3\12212001\I744226A.raw

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3 <110> APPLICANT: OHARA, Osamu
 4 NAGASE, Takahiro
 5 NOMURA, Nobuo
 6 HINUMA, Shuji
 7 FUJII, Ryo
 8 KITAHARA, Osamu
 9 MOGI, Shinichi
 11 <120> TITLE OF INVENTION: Novel G Protein Coupled Receptor Protein and Its DNA
 13 <130> FILE REFERENCE: 2534 USOP
 15 <140> CURRENT APPLICATION NUMBER: US 09/744,226A
 16 <141> CURRENT FILING DATE: 2001-01-22
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP99/03909
 19 <151> PRIOR FILING DATE: 1998-07-22
 21 <150> PRIOR APPLICATION NUMBER: JP 10-207579
 22 <151> PRIOR FILING DATE: 1998-07-23
 24 <150> PRIOR APPLICATION NUMBER: JP 10-225060
 25 <151> PRIOR FILING DATE: 1998-08-07
 27 <150> PRIOR APPLICATION NUMBER: JP 10-284328
 28 <151> PRIOR FILING DATE: 1998-10-06
 30 <160> NUMBER OF SEQ ID NOS: 9
 32 <170> SOFTWARE: PatentIn version 3.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 872
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Homo sapiens
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 45 20 25 30
 47 Asn Leu Thr Pro Gly Gly Lys Asp Ser Ala Ala Arg Ser Leu Asn Lys
 48 35 40 45
 50 Ala Met Val Glu Thr Val Asn Asn Leu Leu Gln Pro Gln Ala Leu Asn
 51 50 55 60
 53 Ala Trp Arg Asp Leu Thr Thr Ser Asp Gln Leu Arg Ala Ala Thr Met
 54 65 70 75 80
 56 Leu Leu His Thr Val Glu Glu Ser Ala Phe Val Leu Ala Asp Asn Leu
 57 85 90 95
 59 Leu Lys Thr Asp Ile Val Arg Glu Asn Thr Asp Asn Ile Lys Leu Glu
 60 100 105 110
 62 Val Ala Arg Leu Ser Thr Glu Gly Asn Leu Glu Asp Leu Lys Phe Pro
 63 115 120 125
 65 Glu Asn Met Gly His Gly Ser Thr Ile Gln Leu Ser Ala Asn Thr Leu
 66 130 135 140
 68 Lys Gln Asn Gly Arg Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr
 69 145 150 155 160
 71 Asn Asn Leu Gly Pro Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu

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74 Gly Thr Glu Ala Leu Ser Thr Asn His Ser Val Ile Val Asn Ser Pro
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77 Val Ile Thr Ala Ala Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu
78          195          200          205
80 Ala Asp Pro Val Val Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu
81          210          215          220
83 Asn Phe Asn Pro Asn Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met
84 225          230          235          240
86 Thr Gly Tyr Trp Ser Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys
87          245          250          255
89 Thr His Thr Thr Cys Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu
90          260          265          270
92 Met Ala His Val Glu Val Lys His Ser Asp Ala Val His Asp Leu Leu
93          275          280          285
95 Leu Asp Val Ile Thr Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu
96          290          295          300
98 Leu Ile Cys Ile Phe Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp
99 305          310          315          320
101 Arg Asn Thr Ile His Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu
102          325          330          335
104 Leu Leu Phe Leu Ile Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys
105          340          345          350
107 Ala Val Phe Ala Ala Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr
108          355          360          365
110 Trp Met Phe Leu Glu Gly Val Gln Leu Tyr Ile Met Leu Val Glu Val
111          370          375          380
113 Phe Glu Ser Glu His Ser Arg Arg Lys Tyr Phe Tyr Leu Val Gly Tyr
114 385          390          395          400
116 Gly Met Pro Ala Leu Ile Val Ala Val Ser Ala Ala Val Asp Tyr Arg
117          405          410          415
119 Ser Tyr Gly Thr Asp Lys Val Cys Trp Leu Arg Leu Asp Thr Tyr Phe
120          420          425          430
122 Ile Trp Ser Phe Ile Gly Pro Ala Thr Leu Ile Ile Met Leu Asn Val
123          435          440          445
125 Ile Phe Leu Gly Ile Ala Leu Tyr Lys Met Phe His His Thr Ala Ile
126          450          455          460
128 Leu Lys Pro Glu Ser Gly Cys Leu Asp Asn Ile Lys Ser Trp Val Ile
129 465          470          475          480
131 Gly Ala Ile Ala Leu Leu Cys Leu Leu Gly Leu Thr Trp Ala Phe Gly
132          485          490          495
134 Leu Met Tyr Ile Asn Glu Ser Thr Val Ile Met Ala Tyr Leu Phe Thr
135          500          505          510
137 Ile Phe Asn Ser Leu Gln Gly Met Phe Ile Phe Ile Phe His Cys Val
138          515          520          525
140 Leu Gln Lys Lys Val Arg Lys Glu Tyr Gly Lys Cys Leu Arg Thr His
141          530          535          540
143 Cys Cys Ser Gly Lys Ser Thr Glu Ser Ser Ile Gly Ser Gly Lys Thr
144 545          550          555          560

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146 Ser Gly Ser Arg Thr Pro Gly Arg Tyr Ser Thr Gly Ser Gln Ser Arg
147          565          570          575
149 Ile Arg Arg Met Trp Asn Asp Thr Val Arg Lys Gln Ser Glu Ser Ser
150          580          585          590
152 Phe Ile Thr Gly Asp Ile Asn Ser Ser Ala Ser Leu Asn Arg Glu Gly
153          595          600          605
155 Leu Leu Asn Asn Ala Arg Asp Thr Ser Val Met Asp Thr Leu Pro Leu
156          610          615          620
158 Asn Gly Asn His Gly Asn Ser Tyr Ser Ile Ala Ser Gly Glu Tyr Leu
159 625          630          635          640
161 Ser Asn Cys Val Gln Ile Ile Asp Arg Gly Tyr Asn His Asn Glu Thr
162          645          650          655
164 Ala Leu Glu Lys Lys Ile Leu Lys Glu Leu Thr Ser Asn Tyr Ile Pro
165          660          665          670
167 Ser Tyr Leu Asn Asn His Glu Arg Ser Ser Glu Gln Asn Arg Asn Leu
168          675          680          685
170 Met Asn Lys Leu Val Asn Asn Leu Gly Ser Gly Arg Glu Asp Asp Ala
171          690          695          700
173 Ile Val Leu Asp Asp Ala Thr Ser Phe Asn His Glu Glu Ser Leu Gly
174 705          710          715          720
176 Leu Glu Leu Ile His Glu Glu Ser Asp Ala Pro Leu Leu Pro Pro Arg
177          725          730          735
179 Val Tyr Ser Thr Glu Asn His Gln Pro His His Tyr Thr Arg Arg Arg
180          740          745          750
182 Ile Pro Gln Asp His Ser Glu Ser Phe Phe Pro Leu Leu Thr Asn Glu
183          755          760          765
185 His Thr Glu Asp Leu Gln Ser Pro His Arg Asp Ser Leu Tyr Thr Ser
186          770          775          780
188 Met Pro Thr Leu Ala Gly Val Ala Ala Thr Glu Ser Val Thr Thr Ser
189 785          790          795          800
191 Thr Gln Thr Glu Pro Pro Ala Lys Cys Gly Asp Ala Glu Asp Val
192          805          810          815
194 Tyr Tyr Lys Ser Met Pro Asn Leu Gly Ser Arg Asn His Val His Gln
195          820          825          830
197 Leu His Thr Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile
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203 Pro Ala His Leu Val Thr Ser Leu
204 865          870
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207 <211> LENGTH: 2616
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 2
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216 agtgcctgcc ggagtttgaa caaggcaatg gtcgagacag ttaacaacct ccttcagcca      180
218 caagctttga atgcatggag agacctgact acgagtgtac agctgcgtgc ggccaccatg      240

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220 ttgcttccata ctgtggagga aagtgtttt gtgtggctg ataacctttt gaagactgac 300
222 attgtcaggg agaatacaga caatattaaa ttggaagttg caagactgag cacagaagga 360
224 aacttagaag acctaaaatt tccagaaaac atgggccatg gaagcaactat ccagctgtct 420
226 gcaaatacct taaagcaaaa tggccgaaat ggagagatca gagtggcctt tgtcctgtat 480
228 aacaacttgg gtcccttattt atccacggag aatgccagta tgaagttggg aacggaagct 540
230 ttgtccacaa atcattctgt tattgtcaat tcccctgtta ttacggcagc aataaacaaa 600
232 gagtccagta acaaggttta ttgggtgat cctgtggtat ttactgttaa acatatcaag 660
234 cagtcagagg aaaatttcaa ccctaactgt tcattttgga gctactccaa gcgtacaatg 720
236 acaggttatt ggtcaacaca aggctgtcgg ctccctgacaa caaataagac acatactaca 780
238 tgctcttgta accacctaac aaattttgca gtactgatgg cacatgtgga agttaagcac 840
240 agtgatgcgg tccatgacct ccttctggat gtgatcagct gggttggaat tttgtgtcc 900
242 cttgtttgtc tccatgattt catcttcaca ttttgccttt tccgcgggct ccagagtgc 960
244 cgtaacacca tccacaagaa cctctgcac agtctctttg tagcagagct gctcttccctg 1020
246 attgggatca accgaactga ccaaccaatt gcctgtgctg ttttgcctgc cctgttttct 1080
248 tcttcttggc tgccctcacc tggatgttcc tggagggggg gcagctttat atacatcatg 1140
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254 gataaagtat gttggctccg acttgacacc tacttcattt ggagttttat aggaccagca 1320
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301 <210> SEQ ID NO: 3

302 <211> LENGTH: 1021

303 <212> TYPE: PRT

304 <213> ORGANISM: Homo sapiens

306 <400> SEQUENCE: 3

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312 20 25 30

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318      50      55      60
320 Leu Cys Met Ile Ser Thr Gly Thr Trp Asn Pro Lys Gly Pro Asp Leu
321 65      70      75      80
323 Ser Asn Cys Thr Ser His Trp Val Asn Gln Leu Ala Gln Lys Ile Arg
324      85      90      95
326 Ser Gly Glu Asn Ala Ala Ser Leu Ala Asn Glu Leu Ala Lys His Thr
327      100     105     110
329 Lys Gly Pro Val Phe Ala Gly Asp Val Ser Ser Ser Val Arg Leu Met
330      115     120     125
332 Glu Gln Leu Val Asp Ile Leu Asp Ala Gln Leu Gln Glu Leu Lys Pro
333      130     135     140
335 Ser Glu Lys Asp Ser Ala Gly Arg Ser Tyr Asn Lys Leu Gln Lys Arg
336 145     150     155     160
338 Glu Lys Thr Cys Arg Ala Tyr Leu Lys Ala Ile Val Asp Thr Val Asp
339      165     170     175
341 Asn Leu Leu Arg Pro Glu Ala Leu Glu Ser Trp Lys His Met Asn Ser
342      180     185     190
344 Ser Glu Gln Ala His Thr Ala Thr Met Leu Leu Asp Thr Leu Glu Glu
345      195     200     205
347 Gly Ala Phe Val Leu Ala Asp Asn Leu Leu Glu Pro Thr Arg Val Ser
348      210     215     220
350 Met Pro Thr Glu Asn Ile Val Leu Glu Val Ala Val Leu Ser Thr Glu
351 225     230     235     240
353 Gly Gln Ile Gln Asp Phe Lys Phe Pro Leu Gly Ile Lys Gly Ala Gly
354      245     250     255
356 Ser Ser Ile Gln Leu Ser Ala Asn Thr Val Lys Gln Asn Ser Arg Asn
357      260     265     270
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362 Leu Ser Thr Glu Asn Ala Thr Ile Lys Leu Gly Ala Asp Phe Ile Gly
363      290     295     300
365 Arg Asn Ser Thr Ile Ala Val Asn Ser His Val Ile Ser Val Ser Ile
366 305     310     315     320
368 Asn Lys Glu Ser Ser Arg Val Tyr Leu Thr Asp Pro Val Leu Phe Thr
369      325     330     335
371 Leu Pro His Ile Asp Pro Asp Asn Tyr Phe Asn Ala Asn Cys Ser Phe
372      340     345     350
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375      355     360     365
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378      370     375     380
380 His Leu Thr Asn Phe Ala Ile Leu Met Ala His Arg Glu Ile Ala Tyr
381 385     390     395     400
383 Lys Asp Gly Val His Glu Leu Leu Leu Thr Val Ile Thr Trp Val Gly
384      405     410     415
386 Ile Val Ile Ser Leu Val Cys Leu Ala Ile Cys Ile Phe Thr Phe Cys

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VERIFICATION SUMMARY

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